A1

underlined portion of the sequence represents the region coding for the leader peptide.

Please delete the paragraph on page 3, lines 11-14, and replace it with the following paragraph:

A2

Figure 2 represents the amino acid sequence (SEQ ID NO: 2) BVH-P7 protein from serotype M1 S. pyogenes strain ATCC700294; SEQ ID NO: 2. The underline sequence represents the 21 amino acid residues leader peptide.

Please delete the paragraph on page 3, lines 16-22, and replace it with the following paragraph:

A3

Figure 3 depicts the comparison of the predicted amino acid sequences of the BVH-P7 open reading frames from Spy74 (SEQ ID NO: 3), Spy70 (SEQ ID NO: 4), Spy69 (SEQ ID NO: 5), Spy68 (SEQ ID NO: 6), Spy 60 (SEQ ID NO: 7), ATCC12357 (SEQ ID NO: 8), ATCC700294 (SEQ ID NO: 2) S. pyogenes strains by using the program Clustal W from MacVector sequence analysis software (version 6.5). Underneath the alignment, there is a consensus line where * and . characters indicate identical and similar amino acid residues, respectively.

Please delete the paragraph on page 27, Table 1, and replace it with the following paragraph:

Table 1. Oligonucleotide primers used for PCR amplifications of S. pyogenes BVH-P7 gene

A4

Genes	Primers I.D.	Restriction site	Vector	Sequence

	(SEQ ID NO)				
BVH-P7	DMAR293 (3)		*NdeI*	pET21b	5'GTAGTCACCCACCATATGGAA GTTTTTAG-3'(SEQ ID NO: 9)
BVH-P7	DMAR294 (4)		*NotI*	pET21b	5'TTTTTTCTTTGCGGCCGCAGT TATTAGT-3'(SEQ ID NO: 10)
BVH-P7	DMAR480a (5)		*BamHI*	pCMV-GH	5'GGGGATCCCACCCACAATCAG G-3'(SEQ ID NO: 11)
BVH-P7	DMAR481a (6)		*SalI*	pCMV-GH	5'GGTTGTCGACAGTAAAGCAAC GCTAGTG-3'(SEQ ID NO: 12)

Please delete the paragraph on page 27, lines 5-15, and replace it with the following paragraph:

It was determined that the 3027-bp including a stop codon (TAA) open reading frame (ORF) of BVH-P7 encodes a 1008 amino-acid-residues polypeptide with a predicted pI of 6.18 and a predicted molecular mass of 111,494.44 Da. Analysis of the predicted amino acid residues sequence (SEQ ID NO :2) using the PSORTII sofware (Real World Computing Partnership (http://psort.nibb.ac.jp)) suggested the existence of a 21 amino acid residues signal peptide (MKKHLKTVALTLTTVSVVTHN)(SEQ ID NO: 13), which ends with a cleavage site situated between an asparagine and a glutamine residues. Analysis of the amino-acid-residues sequence revealed the presence of a cell wall anchoring motif (LPXTGX) (SEQ ID NO: 14) located bewteen residues 974 and 981.